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SEQUENCE LISTING

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OCT 08 2002  
TECH CENTER 1600/2900

<110> BOYLE, WILLIAM J.  
LACEY, DAVID LEE  
CALZONE, FRANK J.  
CHANG, MING-SHI  
SENALDI, GIORGIO

<120> COMBINATION THERAPY FOR CONDITIONS LEADING TO BONE LOSS

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ccggagcaca tttatcacac agcagctgat gaccagtttc tgggtcca 48

&lt;210&gt; 71

&lt;211&gt; 87

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; pAMG21

&lt;400&gt; 71

tatgaaagaa actctgcctc caaaatacct gcattacgat ccggaaactg gtcacacagct 60

gctgtgtgat aaatgtgctc cgggtac 87

&lt;210&gt; 72

&lt;211&gt; 81

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; pAMG21

&lt;400&gt; 72

ccggagcaca tttatcacac agcagctgat gaccagtttc cggatcgtaa tgcaggtatt 60

ttggaggcag agtttctttc a 81

&lt;210&gt; 73

&lt;211&gt; 71

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; pAMG21

&lt;400&gt; 73

gttctcctca tatgaaacat catcaccatc accatcatga aactctgcct ccaaaatacc 60

tgcattacga t 71

&lt;210&gt; 74

&lt;211&gt; 43

&lt;212&gt; DNA

&lt;213&gt; Mus musculus

&lt;400&gt; 74

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 <213> Mus musculus

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 tgaacctgat tcccta 76

<210> 76  
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 <213> Mus musculus

<400> 76  
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<210> 77  
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<400> 77  
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 <213> Homo sapiens

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<210> 79  
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gtttctcctca tatggaaact ctgcctccaa aatacctgca 40

<210> 80

<211> 43

<212> DNA

<213> Mus musculus

<400> 80  
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<210> 81

<211> 18

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<223> pAMG21

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<210> 82

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<210> 83

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> pAMG21

<400> 83

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<210> 84

<211> 30

<212> DNA

<213> Artificial Sequence

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<223> pAMG21

<400> 84

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<210> 85

<211> 12

<212> DNA

<213> Artificial Sequence

<220>

<223> pAMG21

<400> 85

tatgttaatg ag

12

<210> 86

<211> 14

<212> DNA

<213> Artificial Sequence

<220>

<223> pAMG21

<400> 86

gacccctcatt aaca

14

<210> 87

<211> 21

<212> DNA

<213> Artificial Sequence



<220>  
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 <400> 87  
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<210> 88  
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<210> 89  
 <211> 36  
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<220>  
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 <400> 89  
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<210> 90  
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 <212> DNA  
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<220>  
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 <400> 90  
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<210> 91  
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&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; pAMG21

&lt;400&gt; 91

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ctggtcatca gctgctgtgt cataaatgtg ctccgggtac 100

&lt;210&gt; 92

&lt;211&gt; 92

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; pAMG21

&lt;400&gt; 92

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ttggaggcag agtttctttg tcgtcgtcgt cg 92

&lt;210&gt; 93

&lt;211&gt; 26

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; pAMG21-huOPG

&lt;400&gt; 93

acaaacacaa tcgatttgat actaga 26

&lt;210&gt; 94

&lt;211&gt; 50

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; pAMG21-huOPG

<400> 94  
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<210> 95

<211> 50

<212> DNA

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<223> pAMG21-huOPG

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<210> 96

<211> 49

<212> DNA

<213> Artificial Sequence

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<223> pAMG21-huOPG

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<210> 97

<211> 26

<212> DNA

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<223> pAMG21-huOPG

<400> 97  
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<210> 98

<211> 50

<212> DNA

<213> Artificial Sequence

&lt;220&gt;

&lt;223&gt; pAMG21-huOPG

&lt;400&gt; 98

cgcacagcag ctggtgggag gtttcttcgt cgtagtgcag gtatttcggc 50

&lt;210&gt; 99

&lt;211&gt; 49

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; pAMG21-huOPG

&lt;400&gt; 99

gggaagggtt cgtgatggtg atggtgatgc catcctctca tattttatt 49

&lt;210&gt; 100

&lt;211&gt; 50

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; pAMG21-huOPG

&lt;400&gt; 100

cctccttttaa ttagttaaaa caaatctagt atcaaadcga ttgtgtttgt 50

&lt;210&gt; 101

&lt;211&gt; 59

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 101

acaaacacaa tcgatttgat actagatttg ttttaactaa ttaaaggagg aataaaatg 59

&lt;210&gt; 102

&lt;211&gt; 48

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

<400> 102  
ctaattaaag gaggaataaa atgaaagaaa cttttcctcc aaaatatc 48

<210> 103

<211> 31

<212> DNA

<213> Homo sapiens

<400> 103  
tgtttgggta cccggcggac atttatcaca c 31

<210> 104

<211> 59

<212> DNA

<213> Homo sapiens

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<210> 105

<211> 54

<212> DNA

<213> Homo sapiens

<400> 105  
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<210> 106

<211> 31

<212> DNA

<213> Homo sapiens

<400> 106  
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<210> 107

<211> 44

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR primer for Fc-hOPG fusion protein.

<400> 107

cagcccgggt aaaatggaaa cgtttcctcc aaaatatctt catt 44

<210> 108

<211> 44

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR primer for FchOPG fusion protein.

<400> 108

cgtttcatt ttacccgggc tgagcgagag gctcttctgc gtgt 44

<210> 109

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Fc/muOPG

<400> 109

cgctcagccc gggtaaaatg gaaacgttgc ctccaaaata cctgc 45

<210> 110

<211> 39

<212> DNA

<213> Artificial Sequence

<220>

<223> Fc/muOPG

<400> 110

ccattttacc cgggctgagc gagaggctct tctgcgtgt 39

<210> 111

<211> 36

<212> DNA

<213> Artificial Sequence

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<223> muOPG

<400> 111  
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36

<210> 112

<211> 34

<212> DNA

<213> Artificial Sequence

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<223> muOPG

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34

<210> 113

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36

<210> 114

<211> 35

<212> DNA

<213> Artificial Sequence

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<223> huOPG

<400> 114  
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35

&lt;210&gt; 115

&lt;211&gt; 102

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; pAMG21-huOPG

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;223&gt; Linker with XbaI and KpnI sites inserted into human sequence.

&lt;400&gt; 115

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aactagtcac cagctgctgt gtgataaatg tccgccgggt ac 102

&lt;210&gt; 116

&lt;211&gt; 94

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; huOPG

&lt;400&gt; 116

ccggcggaca ttatcacac agcagctgat gactagtttc ttcatacata tgaagatatt 60

ttggagcaaa agtttcata tgttattcct cctt 94

&lt;210&gt; 117

&lt;211&gt; 62

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; huOPG

&lt;400&gt; 117

ctagaaggag gaataacata tggaaacttt tcttgctaaa tatcttcatt atgatgaaga 60

aa 62



<210> 118

<211> 62

<212> DNA

<213> Artificial Sequence

<220>

<223> huOPG

<400> 118

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tt 62

<210> 119

<211> 51

<212> PRT

<213> Homo sapiens

<400> 119

Tyr His Tyr Tyr Asp Gln Asn Gly Arg Met Cys Glu Glu Cys His Met  
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Cys Gln Pro Gly His Phe Leu Val Lys His Cys Lys Gln Pro Lys Arg  
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Asp Thr Val Cys His Lys Pro Cys Glu Pro Gly Val Thr Tyr Thr Asp  
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Asp Trp His  
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<213> Rattus rattus

<220>

<221> CDS

<222> (124)..(1326)

<223>

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aca atg aac aag tgg ctg tgc tgt gca ctc ctg gtg ttc ttg gac atc      168
  Met Asn Lys Trp Leu Cys Cys Ala Leu Leu Val Phe Leu Asp Ile
    1                    5          10          15

att gaa tgg aca acc cag gaa acc ttt cct cca aaa tac ttg cat tat      216
Ile Glu Trp Thr Thr Gln Glu Thr Phe Pro Pro Lys Tyr Leu His Tyr
              20          25          30

gac cca gaa acc gga cgt cag ctc ttg tgt gac aaa tgt gct cct ggc      264
Asp Pro Glu Thr Gly Arg Gln Leu Leu Cys Asp Lys Cys Ala Pro Gly
              35          40          45

acc tac cta aaa cag cac tgc aca gtc agg agg aag aca ctg tgt gtc      312
Thr Tyr Leu Lys Gln His Cys Val Arg Arg Lys Thr Leu Cys Val
    50                    55          60

cct tgc cct gac tac tct tat aca gac agc tgg cac acg agt gat gaa      360
Pro Cys Pro Asp Tyr Ser Tyr Thr Asp Ser Trp His Thr Ser Asp Glu
    65          70          75

tgc gtg tac tgc agc ccc gtg tgc aag gaa ctg cag acc gtg aaa cag      408
Cys Val Tyr Cys Ser Pro Val Cys Lys Glu Leu Gln Thr Val Lys Gln
    80          85          90          95

gag tgc aac cgc acc cac aac cga gtg tgc gaa tgt gag gaa ggg cgc      456
Glu Cys Asn Arg Thr His Asn Arg Val Cys Glu Cys Glu Glu Gly Arg
    100          105          110

tac ctg gag ctc gaa ttc tgc ttg aag cac cgg agc tgt ccc cca ggc      504
Tyr Leu Glu Leu Glu Phe Cys Leu Lys His Arg Ser Cys Pro Pro Gly
    115          120

ttg ggt gtg ctg cag gct ggg acc cca gag cga aac acg gtt tgc aaa      552
Leu Gly Val Leu Gln Ala Gly Thr Pro Glu Arg Asn Thr Val Cys Lys
    130          135          140

aga tgt ccg gat ggg ttc ttc tca ggt gag acg tca tcg aaa gca ccc      600
Arg Cys Pro Asp Gly Phe Phe Ser Gly Glu Thr Ser Ser Lys Ala Pro
    145          150          155

tgt agg aaa cac acc aac tgc agc tca ctt ggc ctc ctg cta att cag      648
Cys Arg Lys His Thr Asn Cys Ser Ser Leu Gly Leu Leu Leu Ile Gln
    160          165          170          175

aaa gga aat gca aca cat gac aat gta tgt tcc gga aac aga gaa gca      696
Lys Gly Asn Ala Thr His Asp Asn Val Cys Ser Gly Asn Arg Glu Ala
    180          185          190

act caa aat tgt gaa ata gat gtc acc ctg tgc gaa gag gca ttc ttc      744
Thr Gln Asn Cys Glu Ile Asp Val Thr Leu Cys Glu Glu Ala Phe Phe
    195          200          205

agg ttt gct gtg cct acc aag att ata ccg aat tgg ctg agt gtt ctg      792
Arg Phe Ala Val Pro Thr Lys Ile Ile Pro Asn Trp Leu Ser Val Leu
    210          215          220

gtg gac agt ttg cct ggg acc aaa gtg aat gca gag agt gta gag agg      840
Val Asp Ser Leu Pro Gly Thr Lys Val Asn Ala Glu Ser Val Glu Arg
    225          230          235

ata aaa cgg aga cac agc tcg caa gag caa act ttc cag cta ctt aag      888
Ile Lys Arg Arg His Ser Ser Gln Glu Gln Thr Phe Gln Leu Leu Lys
    240          245          250          255

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## A-378CIP5 rev.ST25.txt

ctg tgg aag cat caa aac aga gac cag gaa atg gtg aag aag atc atc Leu Trp Lys His Gln Asn Arg Asp Gln Glu Met Val Lys Lys Ile Ile 260 265 270	936
caa gac att gac ctc tgt gaa agc agt gtg caa cgg cat atc ggc cac Gln Asp Ile Asp Leu Cys Glu Ser Ser Val Gln Arg His Ile Gly His 275 280 285	984
gcg aac ctc acc aca gag cag ctc cgc atc ttg atg gag agc ttg cct Ala Asn Leu Thr Thr Glu Gln Leu Arg Ile Leu Met Glu Ser Leu Pro 290 295 300	1032
ggg aag aag atc agc cca gac gag att gag aga acg aga aag acc tgc Gly Lys Lys Ile Ser Pro Asp Glu Ile Glu Arg Thr Arg Lys Thr Cys 305 310 315	1080
aaa ccc agc gag cag ctc ctg aag cta ctg agc ttg tgg agg atc aaa Lys Pro Ser Glu Gln Leu Lys Leu Leu Ser Leu Trp Arg Ile Lys 320 325 330 335	1128
aat gga gac caa gac acc ttg aag ggc ctg atg tac gca ctc aag cac Asn Gly Asp Gln Asp Thr Leu Lys Gly Leu Met Tyr Ala Leu Lys His 340 345 350	1176
ttg aaa gca tac cac ttt ccc aaa acc gtc acc cac agt ctg agg aag Leu Lys Ala Tyr His Phe Pro Lys Thr Val Thr His Ser Leu Arg Lys 355 360 365	1224
acc atc agg ttc ttg cac agc ttc acc atg tac cga ttg tat cag aaa Thr Ile Arg Phe Leu His Ser Phe Thr Met Tyr Arg Leu Tyr Gln Lys 370 375 380	1272
ctc ttt cta gaa atg ata ggg aat cag gtt caa tca gtg aag ata agc Leu Phe Leu Glu Met Ile Gly Asn Gln Val Gln Ser Val Lys Ile Ser 385 390 395	1320
tgc tta tagttaggaa tggtcactgg gctgttttctt caggatgggc caacactgat Cys Leu 400	1376
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gggcactaaa agaaactact atatggagaa agaattgata ttgccccaa cgttcaacaa	2156
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 ctccattgga tctctctgaa tatgggaata tctaacttaa gaagctttga gatttcagtt 2336  
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 aagactatta cagtattgct atttatatcc atccag 2432

<210> 121

<211> 401

<212> PRT

<213> Rattus rattus

<400> 121

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Glu Trp Thr Thr Gln Glu Thr Phe Pro Pro Lys Tyr Leu His Tyr Asp  
 20 25 30

Pro Glu Thr Gly Arg Gln Leu Leu Cys Asp Lys Cys Ala Pro Gly Thr  
 35 40 45

Tyr Leu Lys Gln His Cys Thr Val Arg Arg Lys Thr Leu Cys Val Pro  
 50 55 60

Cys Pro Asp Tyr Ser Tyr Thr Asp Ser Trp His Thr Ser Asp Glu Cys  
 65 70 75 80

Val Tyr Cys Ser Pro Val Cys Lys Glu Leu Gln Thr Val Lys Gln Glu  
 85 90 95

Cys Asn Arg Thr His Asn Arg Val Cys Glu Cys Glu Glu Gly Arg Tyr  
 100 105 110

Leu Glu Leu Glu Phe Cys Leu Lys His Arg Ser Cys Pro Pro Gly Leu  
 115 120 125

Gly Val Leu Gln Ala Gly Thr Pro Glu Arg Asn Thr Val Cys Lys Arg  
 130 135 140

Cys Pro Asp Gly Phe Phe Ser Gly Glu Thr Ser Ser Lys Ala Pro Cys  
 145 150 155 160

Arg Lys His Thr Asn Cys Ser Ser Leu Gly Leu Leu Leu Ile Gln Lys  
 165 170 175

Gly Asn Ala Thr His Asp Asn Val Cys Ser Gly Asn Arg Glu Ala Thr  
 180 185 190

Gln Asn Cys Glu Ile Asp Val Thr Leu Cys Glu Glu Ala Phe Phe Arg  
195 200 205

Phe Ala Val Pro Thr Lys Ile Ile Pro Asn Trp Leu Ser Val Leu Val  
210 215 220

Asp Ser Leu Pro Gly Thr Lys Val Asn Ala Glu Ser Val Glu Arg Ile  
225 230 235 240

Lys Arg Arg His Ser Ser Gln Glu Gln Thr Phe Gln Leu Leu Lys Leu  
245 250 255

Trp Lys His Gln Asn Arg Asp Gln Glu Met Val Lys Lys Ile Ile Gln  
260 265 270

Asp Ile Asp Leu Cys Glu Ser Ser Val Gln Arg His Ile Gly His Ala  
275 280 285

Asn Leu Thr Thr Glu Gln Leu Arg Ile Leu Met Glu Ser Leu Pro Gly  
290 295 300

Lys Lys Ile Ser Pro Asp Glu Ile Glu Arg Thr Arg Lys Thr Cys Lys  
305 310 315 320

Pro Ser Glu Gln Leu Leu Lys Leu Leu Ser Leu Trp Arg Ile Lys Asn  
325 330 335

Gly Asp Gln Asp Thr Leu Lys Gly Leu Met Tyr Ala Leu Lys His Leu  
340 345 350

Lys Ala Tyr His Phe Pro Lys Thr Val Thr His Ser Leu Arg Lys Thr  
355 360 365

Ile Arg Phe Leu His Ser Phe Thr Met Tyr Arg Leu Tyr Gln Lys Leu  
370 375 380

Phe Leu Glu Met Ile Gly Asn Gln Val Gln Ser Val Lys Ile Ser Cys  
385 390 395 400

Leu

<210> 122

<211> 1325

<212> DNA

<213> Mus musculus

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (91)..(1293)

&lt;223&gt;

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (11)..(11)

&lt;223&gt; At position 11, R is a purine.

&lt;400&gt; 122

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gctgcctcct gaggtttccc gaggaccaca atg aac aag tgg ctg tgc tgc gca 114  
 Met Asn Lys Trp Leu Cys Cys Ala  
 1 5

ctc ctg gtg ctc ctg gac atc att gaa tgg aca acc cag gaa acc ctt 162  
 Leu Leu Val Leu Leu Asp Ile Ile Glu Trp Thr Thr Gln Glu Thr Leu  
 10 15 20

ctt cca aag tac ttg cat tat gac cca gaa act ggt cat cag ctc ctg 210  
 Leu Pro Lys Tyr Leu His Tyr Asp Pro Glu Thr Gly His Gln Leu Leu  
 25 30 35 40

tgt gac aaa tgt gct cct ggc acc tac cta aaa cag cac tgc aca gtg 258  
 Cys Asp Lys Cys Ala Pro Gly Thr Tyr Leu Lys Gln His Cys Thr Val  
 45 50 55

agg agg aag aca ttg tgt gtc cct tgc cct gac cac tct tat acg gac 306  
 Arg Arg Lys Thr Leu Cys Val Pro Cys Pro Asp His Ser Tyr Thr Asp  
 60 65 70

agc tgg cac acc agt gat gag tgt gtg tat tgc agc cca gtg tgc aag 354  
 Ser Trp His Thr Ser Asp Glu Cys Val Tyr Cys Ser Pro Val Cys Lys  
 75 80 85

gaa ctg cag tcc gtg aag cag gag tgc aac cgc acc cac aac cga gtg 402  
 Glu Leu Gln Ser Val Lys Gln Glu Cys Asn Arg Thr His Asn Arg Val  
 90 95 100

tgt gag tgt gag gaa ggg cgt tac ctg gag atc gaa ttc tgc ttg aag 450  
 Cys Glu Cys Glu Glu Gly Arg Tyr Leu Glu Ile Glu Phe Cys Leu Lys  
 105 110 115 120

cac cgg agc tgt ccc ccg ggc tcc ggc gtg gtg caa gct gga acc cca 498  
 His Arg Ser Cys Pro Pro Gly Ser Gly Val Val Gln Ala Gly Thr Pro  
 125 130 135

gag cga aac aca gtt tgc aaa aaa tgt cca gat ggg ttc ttc tca ggt 546  
 Glu Arg Asn Thr Val Cys Lys Lys Cys Pro Asp Gly Phe Phe Ser Gly  
 140 145 150

gag act tca tcg aaa gca ccc tgt ata aaa cac acg aac tgc agc aca 594  
 Glu Thr Ser Ser Lys Ala Pro Cys Ile Lys His Thr Asn Cys Ser Thr  
 155 160 165

ttt ggc ctc ctg cta att cag aaa gga aat gca aca cat gac aac tgt 642

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Phe	Gly	Leu	Leu	Leu	Ile	Gln	Lys	Gly	Asn	Ala	Thr	His	Asp	Asn	Cys	
	170					175					180					
tgt	tcc	gga	aac	aga	gaa	gcc	acg	caa	aag	tgt	gga	ata	gat	gtc	acc	690
Cys	Ser	Gly	Asn	Arg	Glu	Ala	Thr	Gln	Lys	Cys	Gly	Ile	Asp	Val	Thr	
185					190					195					200	
ctg	tgt	gaa	gag	gcc	ttc	ttc	agg	ttt	gct	ggt	cct	acc	aag	att	ata	738
Leu	Cys	Glu	Glu	Ala	Phe	Phe	Arg	Phe	Ala	Val	Pro	Thr	Lys	Ile	Ile	
				205					210					215		
cca	aat	tgg	ctg	agt	gtt	ttg	gtg	gac	agt	ttg	cct	ggg	acc	aaa	gtg	786
Pro	Asn	Trp	Leu	Ser	Val	Leu	Val	Asp	Ser	Leu	Pro	Gly	Thr	Lys	Val	
			220					225					230			
aat	gcc	gag	agt	gta	gag	agg	ata	aaa	cgg	aga	cac	agc	tca	caa	gag	834
Asn	Ala	Glu	Ser	Val	Glu	Arg	Ile	Lys	Arg	Arg	His	Ser	Ser	Gln	Glu	
		235					240					245				
caa	acc	ttc	cag	ctg	ctg	aag	ctg	tgg	aaa	cat	caa	aac	aga	gac	cag	882
Gln	Thr	Phe	Gln	Leu	Leu	Lys	Leu	Trp	Lys	His	Gln	Asn	Arg	Asp	Gln	
	250					255					260					
gaa	atg	gtg	aag	aag	atc	atc	caa	gac	att	gac	ctc	tgt	gaa	agc	agc	930
Glu	Met	Val	Lys	Lys	Ile	Ile	Gln	Asp	Ile	Asp	Leu	Cys	Glu	Ser	Ser	
265					270					275					280	
gtg	cag	cgg	cat	ctc	ggc	cac	tcg	aac	ctc	acc	aca	gag	cag	ctt	ctt	978
Val	Gln	Arg	His	Leu	Gly	His	Ser	Asn	Leu	Thr	Thr	Glu	Gln	Leu	Leu	
				285					290					295		
gcc	ttg	atg	gag	agc	ctg	cct	ggg	aag	aag	atc	agc	cca	gaa	gag	att	1026
Ala	Leu	Met	Glu	Ser	Leu	Pro	Gly	Lys	Lys	Ile	Ser	Pro	Glu	Glu	Ile	
			300					305					310			
gag	aga	acg	aga	aag	acc	tgc	aaa	tcg	agc	gag	cag	ctc	ctg	aag	cta	1074
Glu	Arg	Thr	Arg	Lys	Thr	Cys	Lys	Ser	Ser	Glu	Gln	Leu	Leu	Lys	Leu	
		315					320					325				
ctc	agt	tta	tgg	agg	atc	aaa	aat	ggt	gac	caa	gac	acc	ttg	aag	ggc	1122
Leu	Ser	Leu	Trp	Arg	Ile	Lys	Asn	Gly	Asp	Gln	Asp	Thr	Leu	Lys	Gly	
	330					335					340					
ctg	atg	tat	gcc	ctc	aag	cac	ttg	aaa	aca	tcc	cac	ttt	ccc	aaa	act	1170
Leu	Met	Tyr	Ala	Leu	Lys	His	Leu	Lys	Thr	Ser	His	Phe	Pro	Lys	Thr	
345				350					355						360	
gtc	acc	cac	agt	ctg	agg	aag	acc	atg	agg	ttc	ctg	cac	agc	ttc	aca	1218
Val	Thr	His	Ser	Leu	Arg	Lys	Thr	Met	Arg	Phe	Leu	His	Ser	Phe	Thr	
				365				370						375		
atg	tac	aga	ctg	tat	cag	aag	ctc	ttt	tta	gaa	atg	ata	ggg	aat	cag	1266
Met	Tyr	Arg	Leu	Tyr	Gln	Lys	Leu	Phe	Leu	Glu	Met	Ile	Gly	Asn	Gln	
			380					385					390			
gtt	caa	tcc	gtg	aaa	ata	agc	tgc	tta	taactagga	tggtcactgg						1313
Val	Gln	Ser	Val	Lys	Ile	Ser	Cys	Leu								
		395					400									
gctgtttctt	ca															1325
<210>	123															
<211>	401															
<212>	PRT															

&lt;213&gt; Mus musculus

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (11)..(11)

&lt;223&gt; At position 11, R is a purine.

&lt;400&gt; 123

Met Asn Lys Trp Leu Cys Cys Ala Leu Leu Val Leu Leu Asp Ile Ile  
 1 5 10 15

Glu Trp Thr Thr Gln Glu Thr Leu Leu Pro Lys Tyr Leu His Tyr Asp  
 20 25 30

Pro Glu Thr Gly His Gln Leu Leu Cys Asp Lys Cys Ala Pro Gly Thr  
 35 40 45

Tyr Leu Lys Gln His Cys Thr Val Arg Arg Lys Thr Leu Cys Val Pro  
 50 55 60

Cys Pro Asp His Ser Tyr Thr Asp Ser Trp His Thr Ser Asp Glu Cys  
 65 70 75 80

Val Tyr Cys Ser Pro Val Cys Lys Glu Leu Gln Ser Val Lys Gln Glu  
 85 90 95

Cys Asn Arg Thr His Asn Arg Val Cys Glu Cys Glu Glu Gly Arg Tyr  
 100 105 110

Leu Glu Ile Glu Phe Cys Leu Lys His Arg Ser Cys Pro Pro Gly Ser  
 115 120 125

Gly Val Val Gln Ala Gly Thr Pro Glu Arg Asn Thr Val Cys Lys Lys  
 130 135 140

Cys Pro Asp Gly Phe Phe Ser Gly Glu Thr Ser Ser Lys Ala Pro Cys  
 145 150 155 160

Ile Lys His Thr Asn Cys Ser Thr Phe Gly Leu Leu Leu Ile Gln Lys  
 165 170 175

Gly Asn Ala Thr His Asp Asn Cys Cys Ser Gly Asn Arg Glu Ala Thr  
 180 185 190

Gln Lys Cys Gly Ile Asp Val Thr Leu Cys Glu Glu Ala Phe Phe Arg  
 195 200 205

Phe Ala Val Pro Thr Lys Ile Ile Pro Asn Trp Leu Ser Val Leu Val  
 210 215 220



Asp Ser Leu Pro Gly Thr Lys Val Asn Ala Glu Ser Val Glu Arg Ile  
 225 230 235 240  
 Lys Arg Arg His Ser Ser Gln Glu Gln Thr Phe Gln Leu Leu Lys Leu  
 245 250 255  
 Trp Lys His Gln Asn Arg Asp Gln Glu Met Val Lys Lys Ile Ile Gln  
 260 265 270  
 Asp Ile Asp Leu Cys Glu Ser Ser Val Gln Arg His Leu Gly His Ser  
 275 280 285  
 Asn Leu Thr Thr Glu Gln Leu Leu Ala Leu Met Glu Ser Leu Pro Gly  
 290 295 300  
 Lys Lys Ile Ser Pro Glu Glu Ile Glu Arg Thr Arg Lys Thr Cys Lys  
 305 310 315 320  
 Ser Ser Glu Gln Leu Leu Lys Leu Leu Ser Leu Trp Arg Ile Lys Asn  
 325 330 335  
 Gly Asp Gln Asp Thr Leu Lys Gly Leu Met Tyr Ala Leu Lys His Leu  
 340 345 350  
 Lys Thr Ser His Phe Pro Lys Thr Val Thr His Ser Leu Arg Lys Thr  
 355 360 365  
 Met Arg Phe Leu His Ser Phe Thr Met Tyr Arg Leu Tyr Gln Lys Leu  
 370 375 380  
 Phe Leu Glu Met Ile Gly Asn Gln Val Gln Ser Val Lys Ile Ser Cys  
 385 390 395 400

Leu

<210> 124  
 <211> 1356  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (95)..(1297)  
 <223>

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (63)..(63)

&lt;223&gt; At position 63, Y is a pyrimidine.

&lt;400&gt; 124

gtatatataa cgtgatgagc gtacgggtgc ggagacgcac cggcgcgctc gcccagccgc 60

cgycctccaag cccctgaggt ttccggggac caca atg aac aag ttg ctg tgc tgc 115  
 Met Asn Lys Leu Leu Cys Cys  
 1 5

gcg ctc gtg ttt ctg gac atc tcc att aag tgg acc acc cag gaa acg 163  
 Ala Leu Val Phe Leu Asp Ile Ser Ile Lys Trp Thr Thr Gln Glu Thr  
 10 15 20

ttt cct cca aag tac ctt cat tat gac gaa gaa acc tct cat cag ctg 211  
 Phe Pro Pro Lys Tyr Leu His Tyr Asp Glu Glu Thr Ser His Gln Leu  
 25 30 35

ttg tgt gac aaa tgt cct cct ggt acc tac cta aaa caa cac tgt aca 259  
 Leu Cys Asp Lys Cys Pro Pro Gly Thr Tyr Leu Lys Gln His Cys Thr  
 40 45 50 55

gca aag tgg aag tcc gtg tgc gcc cct tgc cct gac cac tac tac aca 307  
 Ala Lys Trp Lys Ser Val Cys Ala Pro Cys Pro Asp His Tyr Tyr Thr  
 60 65 70

gac agc tgg cac acc agt gac gag tgt cta tac tgc agc ccc gtg tgc 355  
 Asp Ser Trp His Thr Ser Asp Glu Cys Leu Tyr Cys Ser Pro Val Cys  
 75 80 85

aag gag ctg cag tac gtc aag cag gag tgc aat cgc acc cac aac cgc 403  
 Lys Glu Leu Gln Tyr Val Lys Gln Glu Cys Asn Arg Thr His Asn Arg  
 90 95 100

gtg tgc gaa tgc aag gaa ggg cgc tac ctt gag ata gag ttc tgc ttg 451  
 Val Cys Glu Cys Lys Glu Gly Arg Tyr Leu Glu Ile Glu Phe Cys Leu  
 105 110 115

aaa cat agg agc tgc cct cct gga ttt gga gtg gtg caa gct gga acc 499  
 Lys His Arg Ser Cys Pro Pro Gly Phe Gly Val Val Gln Ala Gly Thr  
 120 125 130 135

cca gag cga aat aca gtt tgc aaa aga tgt cca gat ggg ttc ttc tca 547  
 Pro Glu Arg Asn Thr Val Cys Lys Arg Cys Pro Asp Gly Phe Phe Ser  
 140 145 150

aat gag acg tca tct aaa gca ccc tgt aga aaa cac aca aat tgc agt 595  
 Asn Glu Thr Ser Ser Lys Ala Pro Cys Arg Lys His Thr Asn Cys Ser  
 155 160 165

gtc ttt ggt ctc ctg cta act cag aaa gga aat gca aca cac gac aac 643  
 Val Phe Gly Leu Leu Leu Thr Gln Lys Gly Asn Ala Thr His Asp Asn  
 170 175 180

ata tgt tcc gga aac agt gaa tca act caa aaa tgt gga ata gat gtt 691  
 Ile Cys Ser Gly Asn Ser Glu Ser Thr Gln Lys Cys Gly Ile Asp Val  
 185 190 195

acc ctg tgt gag gag gca ttc ttc agg ttt gct gtt cct aca aag ttt 739

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Thr 200	Leu	Cys	Glu	Glu	Ala 205	Phe	Phe	Arg	Phe	Ala 210	Val	Pro	Thr	Lys	Phe 215	
acg Thr	cct Pro	aac Asn	tgg Trp	ctt Leu 220	agt Ser	gtc Val	ttg Leu	gta Val	gac Asp 225	aat Asn	ttg Leu	cct Pro	ggc Gly	acc Thr 230	aaa Lys	787
gta Val	aac Asn	gca Ala	gag Glu 235	agt Ser	gta Val	gag Glu	agg Arg	ata Ile 240	aaa Lys	cgg Arg	caa Gln	cac His	agc Ser 245	tca Ser	caa Gln	835
gaa Glu	cag Gln	act Thr 250	ttc Phe	cag Gln	ctg Leu	ctg Leu	aag Lys 255	tta Leu	tgg Trp	aaa Lys	cat His	caa Gln 260	aac Asn	aaa Lys	gcc Ala	883
caa Gln	gat Asp 265	ata Ile	gtc Val	aag Lys	aag Lys	atc Ile 270	atc Ile	caa Gln	gat Asp	att Ile	gac Asp 275	ctc Leu	tgt Cys	gaa Glu	aac Asn	931
agc Ser 280	gtg Val	cag Gln	cgg Arg	cac His	att Ile 285	gga Gly	cat His	gct Ala	aac Asn	ctc Leu 290	acc Thr	ttc Phe	gag Glu	cag Gln	ctt Leu 295	979
cgt Arg	agc Ser	ttg Leu	atg Met	gaa Glu 300	agc Ser	tta Leu	ccg Pro	gga Gly	aag Lys 305	aaa Lys	gtg Val	gga Gly	gca Ala	gaa Glu 310	gac Asp	1027
att Ile	gaa Glu	aaa Lys	aca Thr 315	ata Ile	aag Lys	gca Ala	tgc Cys	aaa Lys 320	ccc Pro	agt Ser	gac Asp	cag Gln	atc Ile 325	ctg Leu	aag Lys	1075
ctg Leu	ctc Leu	agt Ser 330	ttg Leu	tgg Trp	cga Arg	ata Ile	aaa Lys 335	aat Asn	ggc Gly	gac Asp	caa Gln	gac Asp 340	acc Thr	ttg Leu	aag Lys	1123
ggc Gly 345	cta Leu	atg Met	cac His	gca Ala	cta Leu	aag Lys 350	cac His	tca Ser	aag Lys	acg Thr	tac Tyr 355	cac His	ttt Phe	ccc Pro	aaa Lys	1171
act Thr 360	gtc Val	act Thr	cag Gln	agt Ser	cta Leu 365	aag Lys	aag Lys	acc Thr	atc Ile	agg Arg 370	ttc Phe	ctt Leu	cac His	agc Ser	ttc Phe 375	1219
aca Thr	atg Met	tac Tyr	aaa Lys	ttg Leu 380	tat Tyr	cag Gln	aag Lys	tta Leu	ttt Phe 385	tta Leu	gaa Glu	atg Met	ata Ile	ggt Gly 390	aac Asn	1267
cag Gln	gtc Val	caa Gln	tca Ser 395	gta Val	aaa Lys	ata Ile	agc Ser	tgc Cys 400	tta Leu	taactggaaa	tgccattga					1317
gctggtttcct	cacaattggc	gagatcccat	ggatgataa													1356

<210> 125

<211> 401

<212> PRT

<213> Homo sapiens

<220>

<221> misc\_feature

&lt;222&gt; (63)..(63)

&lt;223&gt; At position 63, Y is a pyrimidine.

&lt;400&gt; 125

Met Asn Lys Leu Leu Cys Cys Ala Leu Val Phe Leu Asp Ile Ser Ile  
 1 5 10 15

Lys Trp Thr Thr Gln Glu Thr Phe Pro Pro Lys Tyr Leu His Tyr Asp  
 20 25 30

Glu Glu Thr Ser His Gln Leu Leu Cys Asp Lys Cys Pro Pro Gly Thr  
 35 40 45

Tyr Leu Lys Gln His Cys Thr Ala Lys Trp Lys Ser Val Cys Ala Pro  
 50 55 60

Cys Pro Asp His Tyr Tyr Thr Asp Ser Trp His Thr Ser Asp Glu Cys  
 65 70 75 80

Leu Tyr Cys Ser Pro Val Cys Lys Glu Leu Gln Tyr Val Lys Gln Glu  
 85 90 95

Cys Asn Arg Thr His Asn Arg Val Cys Glu Cys Lys Glu Gly Arg Tyr  
 100 105 110

Leu Glu Ile Glu Phe Cys Leu Lys His Arg Ser Cys Pro Pro Gly Phe  
 115 120 125

Gly Val Val Gln Ala Gly Thr Pro Glu Arg Asn Thr Val Cys Lys Arg  
 130 135 140

Cys Pro Asp Gly Phe Phe Ser Asn Glu Thr Ser Ser Lys Ala Pro Cys  
 145 150 155 160

Arg Lys His Thr Asn Cys Ser Val Phe Gly Leu Leu Leu Thr Gln Lys  
 165 170 175

Gly Asn Ala Thr His Asp Asn Ile Cys Ser Gly Asn Ser Glu Ser Thr  
 180 185 190

Gln Lys Cys Gly Ile Asp Val Thr Leu Cys Glu Glu Ala Phe Phe Arg  
 195 200 205

Phe Ala Val Pro Thr Lys Phe Thr Pro Asn Trp Leu Ser Val Leu Val  
 210 215 220

Asp Asn Leu Pro Gly Thr Lys Val Asn Ala Glu Ser Val Glu Arg Ile  
 225 230 235 240

Lys Arg Gln His Ser Ser Gln Glu Gln Thr Phe Gln Leu Leu Lys Leu  
 245 250 255

Trp Lys His Gln Asn Lys Ala Gln Asp Ile Val Lys Lys Ile Ile Gln  
 260 265 270  
 Asp Ile Asp Leu Cys Glu Asn Ser Val Gln Arg His Ile Gly His Ala  
 275 280 285  
 Asn Leu Thr Phe Glu Gln Leu Arg Ser Leu Met Glu Ser Leu Pro Gly  
 290 295 300  
 Lys Lys Val Gly Ala Glu Asp Ile Glu Lys Thr Ile Lys Ala Cys Lys  
 305 310 315 320  
 Pro Ser Asp Gln Ile Leu Lys Leu Leu Ser Leu Trp Arg Ile Lys Asn  
 325 330 335  
 Gly Asp Gln Asp Thr Leu Lys Gly Leu Met His Ala Leu Lys His Ser  
 340 345 350  
 Lys Thr Tyr His Phe Pro Lys Thr Val Thr Gln Ser Leu Lys Lys Thr  
 355 360 365  
 Ile Arg Phe Leu His Ser Phe Thr Met Tyr Lys Leu Tyr Gln Lys Leu  
 370 375 380  
 Phe Leu Glu Met Ile Gly Asn Gln Val Gln Ser Val Lys Ile Ser Cys  
 385 390 395 400

Leu

<210> 126  
 <211> 139  
 <212> PRT  
 <213> Homo sapiens

<400> 126

Cys Pro Gln Gly Lys Tyr Ile His Pro Gln Asn Asn Ser Ile Cys Cys  
 1 5 10 15  
 Thr Lys Cys His Lys Gly Thr Tyr Leu Tyr Asn Asp Cys Pro Gly Pro  
 20 25 30  
 Gly Gln Asp Thr Asp Cys Arg Glu Cys Glu Ser Gly Ser Phe Thr Ala  
 35 40 45  
 Ser Glu Asn His Leu Arg His Cys Leu Ser Cys Ser Lys Cys Arg Lys  
 50 55 60

Glu Met Gly Gln Val Glu Ile Ser Ser Cys Thr Val Asp Arg Asp Thr  
65 70 75 80

Val Cys Gly Cys Arg Lys Asn Gln Tyr Arg His Tyr Trp Ser Glu Asn  
85 90 95

Leu Phe Gln Cys Phe Asn Cys Ser Leu Cys Leu Asn Gly Thr Val His  
100 105 110

Leu Ser Cys Gln Glu Lys Gln Asn Thr Val Cys Thr Cys His Ala Gly  
115 120 125

Phe Phe Leu Arg Glu Asn Glu Cys Val Ser Cys  
130 135

<210> 127

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> huOPG

<400> 127

acctacttct ttgaagagta gtcgacgaca cactattttac aggcggcc

48

<210> 128

<211> 219

<212> PRT

<213> Rattus rattus

<400> 128

Met Leu Gly Ile Trp Thr Leu Leu Pro Leu Val Leu Thr Ser Val Ala  
1 5 10 15

Arg Leu Ser Ser Lys Ser Val Asn Ala Gln Val Thr Asp Ile Asn Ser  
20 25 30

Lys Gly Leu Glu Leu Arg Lys Thr Val Thr Thr Val Glu Thr Gln Asn  
35 40 45

Leu Glu Gly Leu His His Asp Gly Gln Phe Cys His Lys Pro Cys Pro  
50 55 60

Pro Gly Glu Arg Lys Ala Arg Asp Cys Thr Val Asn Gly Asp Glu Pro  
65 70 75 80

Asp Cys Val Pro Cys Gln Glu Gly Lys Glu Tyr Thr Asp Lys Ala His  
85 90 95

Phe Ser Ser Lys Cys Arg Arg Cys Arg Leu Cys Asp Glu Gly His Gly  
100 105 110

Leu Glu Val Glu Ile Asn Cys Thr Arg Thr Gln Asn Thr Lys Cys Arg  
115 120 125

Cys Lys Pro Asn Phe Phe Cys Asn Ser Thr Val Cys Glu His Cys Asp  
130 135 140

Pro Cys Thr Lys Cys Glu His Gly Ile Ile Lys Glu Cys Thr Leu Thr  
145 150 155 160

Ser Asn Thr Lys Cys Lys Glu Glu Gly Ser Arg Ser Asn Leu Gly Trp  
165 170 175

Leu Cys Leu Leu Leu Leu Pro Ile Pro Leu Ile Val Trp Val Lys Arg  
180 185 190

Lys Glu Val Gln Lys Thr Cys Arg Lys His Arg Lys Glu Asn Gln Gly  
195 200 205

Ser His Glu Ser Pro Thr Leu Asn Pro Glu Thr  
210 215

<210> 129

<211> 280

<212> PRT

<213> Rattus rattus

<400> 129

Met Gly Leu Ser Thr Val Pro Asp Leu Leu Leu Pro Leu Val Leu Leu  
1 5 10 15

Glu Leu Leu Val Gly Ile Tyr Pro Ser Gly Val Ile Gly Leu Val Pro  
20 25 30

His Leu Gly Asp Arg Glu Lys Arg Asp Ser Val Cys Pro Gln Gly Lys  
35 40 45

Tyr Ile His Pro Gln Asn Asn Ser Ile Cys Cys Thr Lys Cys His Lys  
50 55 60

Gly Thr Tyr Leu Tyr Asn Asp Cys Pro Gly Pro Gly Gln Asp Thr Asp  
65 70 75 80

Cys Arg Glu Cys Glu Ser Gly Ser Phe Thr Ala Ser Glu Asn His Leu  
85 90 95

Arg His Cys Leu Ser Cys Ser Lys Cys Arg Lys Glu Met Gly Gln Val  
100 105 110

Glu Ile Ser Ser Cys Thr Val Asp Arg Asp Thr Val Cys Gly Cys Arg  
115 120 125

Lys Asn Gln Tyr Arg His Tyr Trp Ser Glu Asn Leu Phe Gln Cys Phe  
130 135 140

Asn Cys Ser Leu Cys Leu Asn Gly Thr Val His Leu Ser Cys Gln Glu  
145 150 155 160

Lys Gln Asn Thr Val Cys Thr Cys His Ala Gly Phe Phe Leu Arg Glu  
165 170 175

Asn Glu Cys Val Ser Cys Ser Asn Cys Lys Lys Ser Leu Glu Cys Thr  
180 185 190

Lys Leu Cys Leu Pro Gln Ile Glu Asn Val Lys Gly Thr Glu Asp Ser  
195 200 205

Gly Thr Thr Val Leu Leu Pro Leu Val Ile Phe Phe Gly Leu Cys Leu  
210 215 220

Leu Ser Leu Leu Phe Ile Gly Leu Met Thr Arg Thr Gln Arg Trp Lys  
225 230 235 240

Ser Lys Leu Tyr Ser Ile Val Cys Gly Lys Ser Thr Pro Glu Lys Glu  
245 250 255

Gly Glu Leu Glu Gly Thr Thr Thr Lys Pro Leu Ala Pro Asn Pro Ser  
260 265 270

Phe Ser Pro Thr Pro Gly Phe Thr  
275 280

<210> 130

<211> 207

<212> PRT

<213> Rattus rattus

<400> 130



Met Leu Arg Leu Ile Ala Leu Leu Val Cys Val Val Tyr Val Tyr Gly  
1 5 10 15

Asp Asp Val Pro Tyr Ser Ser Asn Gln Gly Lys Cys Gly Gly His Asp  
20 25 30

Tyr Glu Lys Asp Gly Leu Cys Cys Ala Ser Cys His Pro Gly Phe Tyr  
35 40 45

Ala Ser Arg Leu Cys Gly Pro Gly Ser Asn Thr Val Cys Ser Pro Cys  
50 55 60

Glu Asp Gly Thr Phe Thr Ala Ser Thr Asn His Ala Pro Ala Cys Val  
65 70 75 80

Ser Cys Arg Gly Pro Cys Thr Gly His Leu Ser Glu Ser Gln Pro Cys  
85 90 95

Asp Arg Thr His Asp Arg Val Cys Asn Cys Ser Thr Gly Asn Tyr Cys  
100 105 110

Leu Leu Lys Gly Gln Asn Gly Cys Arg Ile Cys Ala Pro Gln Thr Lys  
115 120 125

Cys Pro Ala Gly Tyr Gly Val Ser Gly His Thr Arg Ala Gly Asp Thr  
130 135 140

Leu Cys Glu Lys Cys Pro Pro His Thr Tyr Ser Asp Ser Leu Ser Pro  
145 150 155 160

Thr Glu Arg Cys Gly Thr Ser Phe Asn Tyr Ile Ser Val Gly Phe Asn  
165 170 175

Leu Tyr Pro Val Asn Glu Thr Ser Cys Thr Thr Thr Ala Gly His Asn  
180 185 190

Glu Val Ile Lys Thr Lys Glu Phe Thr Val Thr Leu Asn Tyr Thr  
195 200 205

<210> 131

<211> 227

<212> PRT

<213> Rattus rattus

<400> 131

Met Ala Pro Val Ala Val Trp Ala Ala Leu Ala Val Gly Leu Glu Leu  
1 5 10 15

Trp Ala Ala Ala His Ala Leu Pro Ala Gln Val Ala Phe Thr Pro Tyr  
 20 25 30

Ala Pro Glu Pro Gly Ser Thr Cys Arg Leu Arg Glu Thr Thr Asp Gln  
 35 40 45

Thr Ala Gln Met Cys Cys Ser Lys Cys Ser Pro Gly Gln His Ala Lys  
 50 55 60

Val Phe Cys Thr Lys Thr Ser Asp Thr Val Cys Asp Ser Cys Glu Asp  
 65 70 75 80

Ser Thr Tyr Thr Gln Leu Trp Asn Trp Val Pro Glu Cys Leu Ser Cys  
 85 90 95

Gly Ser Arg Cys Ser Ser Asp Gln Val Glu Thr Gln Ala Cys Thr Arg  
 100 105 110

Glu Gln Asn Arg Ile Cys Thr Cys Arg Pro Gly Trp Tyr Cys Ala Leu  
 115 120 125

Ser Lys Gln Glu Gly Cys Arg Leu Cys Ala Pro Leu Arg Lys Cys Arg  
 130 135 140

Pro Gly Phe Gly Val Ala Arg Pro Gly Thr Glu Thr Ser Asp Val Val  
 145 150 155 160

Cys Lys Pro Cys Ala Pro Gly Thr Phe Ser Asn Thr Thr Ser Ser Thr  
 165 170 175

Asp Ile Cys Arg Pro His Gln Ile Cys Asn Val Val Ala Ile Pro Gly  
 180 185 190

Asn Ala Ser Arg Asp Ala Val Cys Thr Ser Thr Ser Pro Thr Arg Ser  
 195 200 205

Met Ala Pro Gly Ala Val His Leu Pro Gln Pro Val Ser Thr Arg Ser  
 210 215 220

Gln His Thr  
 225

<210> 132

<211> 197

<212> PRT

<213> Rattus rattus

<400> 132

Met Val Ser Leu Pro Arg Leu Cys Ala Leu Trp Gly Cys Leu Leu Thr  
1 5 10 15

Ala Val His Leu Gly Gln Cys Val Thr Cys Ser Asp Lys Gln Tyr Leu  
20 25 30

His Asp Gly Gln Cys Cys Asp Leu Cys Gln Pro Gly Ser Arg Leu Thr  
35 40 45

Ser His Cys Thr Ala Leu Glu Lys Thr Gln Cys His Pro Cys Asp Ser  
50 55 60

Gly Glu Phe Ser Ala Gln Trp Asn Arg Glu Ile Arg Cys His Gln His  
65 70 75 80

Arg His Cys Glu Pro Asn Gln Gly Leu Arg Val Lys Lys Glu Gly Thr  
85 90 95

Ala Glu Ser Asp Thr Val Cys Thr Cys Lys Glu Gly Gln His Cys Thr  
100 105 110

Ser Lys Asp Cys Glu Ala Cys Ala Gln His Thr Pro Cys Ile Pro Gly  
115 120 125

Phe Gly Val Met Glu Met Ala Thr Glu Thr Thr Asp Thr Val Cys His  
130 135 140

Pro Cys Pro Val Gly Phe Phe Ser Asn Gln Ser Ser Leu Phe Glu Lys  
145 150 155 160

Cys Tyr Pro Trp Thr Ser Cys Glu Asp Lys Asn Leu Glu Val Leu Gln  
165 170 175

Lys Gly Thr Ser Gln Thr Asn Val Ile Cys Gly Leu Lys Ser Arg Met  
180 185 190

Arg Ala Leu Leu Val  
195

<210> 133

<211> 208

<212> PRT

<213> Rattus rattus

<400> 133

Met Asn Lys Trp Leu Cys Cys Ala Leu Leu Val Phe Leu Asp Ile Ile  
1 5 10 15

Glu Trp Thr Thr Gln Glu Thr Phe Pro Pro Lys Tyr Leu His Tyr Asp  
20 25 30

Pro Glu Thr Gly Arg Gln Leu Leu Cys Asp Lys Cys Ala Pro Gly Thr  
35 40 45

Tyr Leu Lys Gln His Cys Thr Val Arg Arg Lys Thr Leu Cys Val Pro  
50 55 60

Cys Pro Asp Tyr Ser Tyr Thr Asp Ser Trp His Thr Ser Asp Glu Cys  
65 70 75 80

Val Tyr Cys Ser Pro Val Cys Lys Glu Leu Gln Thr Val Lys Gln Glu  
85 90 95

Cys Asn Arg Thr His Asn Arg Val Cys Glu Cys Glu Glu Gly Arg Tyr  
100 105 110

Leu Glu Leu Glu Phe Cys Leu Lys His Arg Ser Cys Pro Pro Gly Leu  
115 120 125

Gly Val Leu Gln Ala Gly Thr Pro Glu Arg Asn Thr Val Cys Lys Arg  
130 135 140

Cys Pro Asp Gly Phe Phe Ser Gly Glu Thr Ser Ser Lys Ala Pro Cys  
145 150 155 160

Arg Lys His Thr Asn Cys Ser Ser Leu Gly Leu Leu Leu Ile Gln Lys  
165 170 175

Gly Asn Ala Thr His Asp Asn Val Cys Ser Gly Asn Arg Glu Ala Thr  
180 185 190

Gln Asn Cys Gly Ile Asp Val Thr Leu Cys Glu Glu Ala Phe Phe Arg  
195 200 205

<210> 134

<211> 224

<212> PRT

<213> Rattus rattus

<400> 134

Met Gly Ala Gly Ala Thr Gly Arg Ala Met Asp Gly Pro Arg Leu Leu  
1 5 10 15

Leu Leu Leu Leu Leu Gly Val Ser Leu Gly Gly Ala Lys Glu Ala Cys  
20 25 30

Pro Thr Gly Leu Tyr Thr His Ser Gly Glu Cys Cys Lys Ala Cys Asn  
 35 40 45

Leu Gly Glu Gly Val Ala Gln Pro Cys Gly Ala Asn Gln Thr Val Cys  
 50 55 60

Glu Pro Cys Leu Asp Ser Val Thr Phe Ser Asp Val Val Ser Ala Thr  
 65 70 75 80

Glu Pro Cys Lys Pro Cys Thr Glu Cys Val Gly Leu Gln Ser Met Ser  
 85 90 95

Ala Pro Cys Val Glu Ala Asp Asp Ala Val Cys Arg Cys Ala Tyr Gly  
 100 105 110

Tyr Tyr Gln Asp Glu Thr Thr Gly Arg Cys Glu Ala Cys Arg Val Cys  
 115 120 125

Glu Ala Gly Ser Gly Leu Val Phe Ser Cys Gln Asp Lys Gln Asn Thr  
 130 135 140

Val Cys Glu Glu Cys Pro Asp Gly Thr Tyr Ser Asp Glu Ala Asn His  
 145 150 155 160

Val Asp Pro Cys Leu Pro Cys Thr Val Cys Glu Asp Thr Glu Arg Gln  
 165 170 175

Leu Arg Glu Cys Thr Arg Trp Ala Asp Ala Glu Cys Glu Glu Ile Pro  
 180 185 190

Gly Arg Trp Ile Thr Arg Ser Thr Pro Pro Glu Gly Ser Asp Ser Thr  
 195 200 205

Ala Pro Ser Thr Gln Glu Pro Glu Ala Pro Pro Glu Gln Asp Leu Ile  
 210 215 220

<210> 135

<211> 202

<212> PRT

<213> Rattus rattus

<400> 135

Met Tyr Val Trp Val Gln Gln Pro Thr Ala Phe Leu Leu Leu Gly Leu  
 1 5 10 15

Ser Leu Gly Val Thr Val Lys Leu Asn Cys Val Lys Asp Thr Tyr Pro  
 20 25 30

Ser Gly His Lys Cys Cys Arg Glu Cys Gln Pro Gly His Gly Met Val  
 35 40 45

Ser Arg Cys Asp His Thr Arg Asp Thr Val Cys His Pro Cys Glu Pro  
 50 55 60

Gly Phe Tyr Asn Glu Ala Val Asn Tyr Asp Thr Cys Lys Gln Cys Thr  
 65 70 75 80

Gln Cys Asn His Arg Ser Gly Ser Glu Leu Lys Gln Asn Cys Thr Pro  
 85 90 95

Thr Glu Asp Thr Val Cys Gln Cys Arg Pro Gly Thr Gln Pro Arg Gln  
 100 105 110

Asp Ser Ser His Lys Leu Gly Val Asp Cys Val Pro Cys Pro Pro Gly  
 115 120 125

His Phe Ser Pro Gly Ser Asn Gln Ala Cys Lys Pro Trp Thr Asn Cys  
 130 135 140

Thr Leu Ser Gly Lys Gln Ile Arg His Pro Ala Ser Asn Ser Val Cys  
 145 150 155 160

Glu Asp Arg Ser Leu Leu Ala Thr Leu Leu Trp Glu Thr Gln Arg Thr  
 165 170 175

Thr Phe Arg Pro Thr Thr Val Pro Ser Thr Thr Val Trp Pro Arg Thr  
 180 185 190

Ser Gln Leu Pro Ser Thr Pro Thr Leu Val  
 195 200

<210> 136

<211> 191

<212> PRT

<213> Rattus rattus

<400> 136

Met Gly Asn Asn Cys Tyr Asn Val Val Val Ile Val Leu Leu Leu Val  
 1 5 10 15

Gly Cys Glu Lys Val Gly Ala Val Gln Asn Ser Cys Asp Asn Cys Gln  
 20 25 30

Pro Gly Thr Phe Cys Arg Lys Tyr Asn Pro Val Cys Lys Ser Cys Pro  
 35 40 45

Pro Ser Thr Phe Ser Ser Ile Gly Gly Gln Pro Asn Cys Asn Ile Cys  
50 55 60

Arg Val Cys Ala Gly Tyr Phe Arg Phe Lys Lys Phe Cys Ser Ser Thr  
65 70 75 80

His Asn Ala Glu Cys Glu Cys Ile Glu Gly Phe His Cys Leu Gly Pro  
85 90 95

Gln Cys Thr Arg Cys Glu Lys Asp Cys Arg Pro Gly Gln Glu Leu Thr  
100 105 110

Lys Gln Gly Cys Lys Thr Cys Ser Leu Gly Thr Phe Asn Asp Gln Asn  
115 120 125

Gly Thr Gly Val Cys Arg Pro Trp Thr Asn Cys Ser Leu Asp Gly Arg  
130 135 140

Ser Val Leu Lys Thr Gly Thr Thr Glu Lys Asp Val Val Cys Gly Pro  
145 150 155 160

Pro Val Val Ser Phe Ser Pro Ser Thr Thr Ile Ser Val Thr Pro Glu  
165 170 175

Gly Gly Pro Gly Gly His Ser Leu Gln Val Leu Thr Leu Phe Leu  
180 185 190

<210> 137

<211> 54

<212> DNA

<213> Artificial Sequence

<220>

<223> huOPG

<400> 137

tatggatgaa gaaacttctc atcagctgct gtgtgataaa tgtccgccgg gtac

54

<210> 138

<211> 120

<212> PRT

<213> Homo sapiens

<400> 138

His Ala Leu Pro Ala Gln Val Ala Phe Thr Pro Tyr Ala Pro Glu Pro  
1 5 10 15

Gly Ser Thr Cys Arg Leu Arg Glu Tyr Tyr Asp Gln Thr Ala Gln Met  
20 25 30  
Cys Cys Ser Lys Cys Ser Pro Gly Gln His Ala Lys Val Phe Cys Thr  
35 40 45  
Lys Thr Ser Asp Thr Val Cys Asp Ser Cys Glu Asp Ser Thr Tyr Thr  
50 55 60  
Gln Leu Trp Asn Trp Val Pro Glu Cys Leu Ser Cys Gly Ser Arg Cys  
65 70 75 80  
Ser Ser Asp Gln Val Glu Thr Gln Ala Cys Thr Arg Glu Gln Asn Arg  
85 90 95  
Ile Cys Thr Cys Arg Pro Gly Trp Tyr Cys Ala Leu Ser Lys Gln Glu  
100 105 110  
Gly Cys Arg Leu Cys Ala Pro Leu  
115 120

<210> 139

<211> 380

<212> PRT

<213> Homo sapiens

<400> 139

Glu Thr Phe Pro Pro Lys Tyr Leu His Tyr Asp Glu Glu Thr Ser His  
1 5 10 15  
Gln Leu Leu Cys Asp Lys Cys Pro Pro Gly Thr Tyr Leu Lys Gln His  
20 25 30  
Cys Thr Ala Lys Trp Lys Thr Val Cys Ala Pro Cys Pro Asp His Tyr  
35 40 45  
Tyr Thr Asp Ser Trp His Thr Ser Asp Glu Cys Leu Tyr Cys Ser Pro  
50 55 60  
Val Cys Lys Glu Leu Gln Tyr Val Lys Gln Glu Cys Asn Arg Thr His  
65 70 75 80  
Asn Arg Val Cys Glu Cys Lys Glu Gly Arg Tyr Leu Glu Ile Glu Phe  
85 90 95  
Cys Leu Lys His Arg Ser Cys Pro Pro Gly Phe Gly Val Val Gln Ala  
100 105 110



Gly Thr Pro Glu Arg Asn Thr Val Cys Lys Arg Cys Pro Asp Gly Phe  
 115 120 125  
 Phe Ser Asn Glu Thr Ser Ser Lys Ala Pro Cys Arg Lys His Thr Asn  
 130 135 140  
 Cys Ser Val Phe Gly Leu Leu Leu Thr Gln Lys Gly Asn Ala Thr His  
 145 150 155 160  
 Asp Asn Ile Cys Ser Gly Asn Ser Glu Ser Thr Gln Lys Cys Gly Ile  
 165 170 175  
 Asp Val Thr Leu Cys Glu Glu Ala Phe Phe Arg Phe Ala Val Pro Thr  
 180 185 190  
 Lys Phe Thr Pro Asn Trp Leu Ser Val Leu Val Asp Asn Leu Pro Gly  
 195 200 205  
 Thr Lys Val Asn Ala Glu Ser Val Glu Arg Ile Lys Arg Gln His Ser  
 210 215 220  
 Ser Gln Glu Gln Thr Phe Gln Leu Leu Lys Leu Trp Lys His Gln Asn  
 225 230 235 240  
 Lys Ala Gln Asp Ile Val Lys Lys Ile Ile Gln Asp Ile Asp Leu Cys  
 245 250 255  
 Glu Asn Ser Val Gln Arg His Ile Gly His Ala Asn Leu Thr Phe Glu  
 260 265 270  
 Gln Leu Arg Ser Leu Met Glu Ser Leu Pro Gly Lys Lys Val Gly Ala  
 275 280 285  
 Glu Asp Ile Glu Lys Thr Ile Lys Ala Cys Lys Pro Ser Asp Gln Ile  
 290 295 300  
 Leu Lys Leu Leu Ser Leu Trp Arg Ile Lys Asn Gly Asp Gln Asp Thr  
 305 310 315 320  
 Leu Lys Gly Leu Met His Ala Leu Lys His Ser Lys Thr Lys His Phe  
 325 330 335  
 Pro Lys Thr Val Thr Gln Ser Leu Lys Lys Thr Ile Arg Phe Leu His  
 340 345 350  
 Ser Phe Thr Met Tyr Lys Leu Tyr Gln Lys Leu Phe Leu Glu Met Ile  
 355 360 365  
 Gly Asn Gln Val Gln Ser Val Lys Ile Ser Cys Leu  
 370 375 380

<210> 140  
 <211> 30  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> huOPG  
 <400> 140  
 tggaccaccc agaagtacct tcattatgac 30  
  
 <210> 141  
 <211> 30  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> huOPG  
 <400> 141  
 gtcataatga aggtacttct gggtggtcca 30  
  
 <210> 142  
 <211> 31  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> huOPG  
 <400> 142  
 ggaccaccca gcttcattat gacgaagaaa c 31  
  
 <210> 143  
 <211> 31  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>

<223> huOPG  
 <400> 143  
 gtttcttcgt cataatgaag ctgggtgggc c 31  
 <210> 144  
 <211> 29  
 <212> DNA  
 <213> Artificial Sequence  
 <220>  
 <223> huOPG  
 <400> 144  
 gtggaccacc caggacgaag aaacctctc 29  
 <210> 145  
 <211> 29  
 <212> DNA  
 <213> Artificial Sequence  
 <220>  
 <223> huOPG  
 <400> 145  
 gagaggtttc ttcgtcctgg gtggtccac 29  
 <210> 146  
 <211> 29  
 <212> DNA  
 <213> Artificial Sequence  
 <220>  
 <223> huOPG  
 <400> 146  
 cgtttcctcc aaagttcctt cattatgac 29  
 <210> 147  
 <211> 29  
 <212> DNA  
 <213> Artificial Sequence

<220>

<223> huOPG

<400> 147

gtcataatga aggaactttg gaggaaacg

29

<210> 148

<211> 32

<212> DNA

<213> Artificial Sequence

<220>

<223> huOPG

<400> 148

ggaaacgttt cctgcaaagt accttcatta tg

32

<210> 149

<211> 32

<212> DNA

<213> Artificial Sequence

<220>

<223> huOPG

<400> 149

cataatgaag gtactttgca ggaaacgttt cc

32

<210> 150

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> muOPG

<400> 150

cacgcaaaag tcgggaatag atgtcac

27

<210> 151

<211> 27

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; muOPG

&lt;400&gt; 151

gtgacatcta ttcccgactt ttgcgtg

27

&lt;210&gt; 152

&lt;211&gt; 25

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; muOPG

&lt;400&gt; 152

caccctgtcg gaagaggcct tcttc

25

&lt;210&gt; 153

&lt;211&gt; 25

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; muOPG

&lt;400&gt; 153

gaagaaggcc tcttccgaca gggtg

25

&lt;210&gt; 154

&lt;211&gt; 24

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; muOPG

&lt;400&gt; 154

tgacctctcg gaaagcagcg tgca

24

<210> 155

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> muOPG

<400> 155

tgcacgctgc tttccgagag gtca

24

<210> 156

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> muOPG

<400> 156

cctcgaaatc gagcgagcag ctcc

24

<210> 157

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> muOPG

<400> 157

cgatttcgag gtctttctcg ttctc

25

<210> 158

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> muOPG

<400> 158  
ccgtgaaaat aagctcgta taactaggaa tgg 33

<210> 159

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> muOPG

<400> 159  
ccattcctag ttataacgag cttattttca cgg 33

<210> 160

<211> 38

<212> DNA

<213> Artificial Sequence

<220>

<223> muOPG

<400> 160  
cctctgagct caagcttccg aggaccacaa tgaacaag 38

<210> 161

<211> 44

<212> DNA

<213> Artificial Sequence

<220>

<223> muOPG

<400> 161  
cctctctcga gtcaggtgac atctattcca cacttttgcg tggc 44

<210> 162

<211> 38

<212> DNA

<213> Artificial Sequence

<220>

<223> muOPG

<400> 162

cctctgagct caagcttccg aggaccacaa tgaacaag

38

<210> 163

<211> 38

<212> DNA

<213> Artificial Sequence

<220>

<223> muOPG

<400> 163

cctctctcga gtcaaggaac agcaaacctg aagaaggc

38

<210> 164

<211> 38

<212> DNA

<213> Artificial Sequence

<220>

<223> muOPG

<400> 164

cctctgagct caagcttccg aggaccacaa tgaacaag

38

<210> 165

<211> 38

<212> DNA

<213> Artificial Sequence

<220>

<223> muOPG

<400> 165

cctctctcga gtcactctgt ggtgaggttc gagtggcc

38

<210> 166

<211> 38

<212> DNA



<213> Artificial Sequence

<220>

<223> muOPG

<400> 166  
cctctgagct caagcttccg aggaccacaa tgaacaag

38

<210> 167

<211> 38

<212> DNA

<213> Artificial Sequence

<220>

<223> muOPG

<400> 167  
cctctctcga gtcaggatgt tttcaagtgc ttgagggc

38

<210> 168

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> pAMG22

<400> 168

Met	Lys	His	His	His	His	His	His	His	Ala	Ser	Val	Asn	Ala	Leu	Glu
1				5					10					15	

<210> 169

<211> 70

<212> PRT

<213> Homo sapiens

<400> 169

Ala	Leu	Leu	Val	Phe	Leu	Asp	Ile	Ile	Glu	Trp	Thr	Thr	Gln	Glu	Thr
1				5					10					15	

Phe	Pro	Pro	Lys	Tyr	Leu	His	Tyr	Asp	Pro	Glu	Thr	Gly	Arg	Gln	Leu
			20					25					30		

Leu Cys Asp Lys Cys Ala Pro Gly Thr Tyr Leu Lys Gln His Cys Thr  
 35 40 45

Val Arg Arg Lys Thr Leu Cys Val Pro Cys Pro Asp Tyr Ser Tyr Thr  
 50 55 60

Asp Ser Trp His Thr Ser  
 65 70

<210> 170

<211> 48

<212> PRT

<213> Homo sapiens

<400> 170

Tyr Leu His Tyr Asp Pro Glu Thr Gly Arg Gln Leu Leu Cys Asp Lys  
 1 5 10 15

Cys Ala Pro Gly Thr Tyr Leu Lys Gln His Cys Thr Val Arg Arg Lys  
 20 25 30

Thr Leu Cys Val Pro Cys Pro Asp Tyr Ser Tyr Thr Asp Ser Trp His  
 35 40 45

<210> 171

<211> 401

<212> PRT

<213> Mus musculus

<400> 171

Met Asn Lys Trp Leu Cys Cys Ala Leu Leu Val Leu Leu Asp Ile Ile  
 1 5 10 15

Glu Trp Thr Thr Gln Glu Thr Leu Pro Pro Lys Tyr Leu His Tyr Asp  
 20 25 30

Pro Glu Thr Gly His Gln Leu Leu Cys Asp Lys Cys Ala Pro Gly Thr  
 35 40 45

Tyr Leu Lys Gln His Cys Thr Val Arg Arg Lys Thr Leu Cys Val Pro  
 50 55 60

Cys Pro Asp His Ser Tyr Thr Asp Ser Trp His Thr Ser Asp Glu Cys  
 65 70 75 80

Val Tyr Cys Ser Pro Val Cys Lys Glu Leu Gln Ser Val Lys Gln Glu  
 85 90 95  
 Cys Asn Arg Thr His Asn Arg Val Cys Glu Cys Glu Glu Gly Arg Tyr  
 100 105 110  
 Leu Glu Ile Glu Phe Cys Leu Lys His Arg Ser Cys Pro Pro Gly Ser  
 115 120 125  
 Gly Val Val Gln Ala Gly Thr Pro Glu Arg Asn Thr Val Cys Lys Lys  
 130 135 140  
 Cys Pro Asp Gly Phe Phe Ser Gly Glu Thr Ser Ser Lys Ala Pro Cys  
 145 150 155 160  
 Ile Lys His Thr Asn Cys Ser Thr Phe Gly Leu Leu Leu Ile Gln Lys  
 165 170 175  
 Gly Asn Ala Thr His Asp Asn Val Cys Ser Gly Asn Arg Glu Ala Thr  
 180 185 190  
 Gln Lys Cys Gly Ile Asp Val Thr Leu Cys Glu Glu Ala Phe Phe Arg  
 195 200 205  
 Phe Ala Val Pro Thr Lys Ile Ile Pro Asn Trp Leu Ser Val Leu Val  
 210 215 220  
 Asp Ser Leu Pro Gly Thr Lys Val Asn Ala Glu Ser Val Glu Arg Ile  
 225 230 235 240  
 Lys Arg Arg His Ser Ser Gln Glu Gln Thr Phe Gln Leu Leu Lys Leu  
 245 250 255  
 Trp Lys His Gln Asn Arg Asp Gln Glu Met Val Lys Lys Ile Ile Gln  
 260 265 270  
 Asp Ile Asp Leu Cys Glu Ser Ser Val Gln Arg His Leu Gly His Ser  
 275 280 285  
 Asn Leu Thr Thr Glu Gln Leu Leu Ala Leu Met Glu Ser Leu Pro Gly  
 290 295 300  
 Lys Lys Ile Ser Pro Glu Glu Ile Glu Arg Thr Arg Lys Thr Cys Lys  
 305 310 315 320  
 Ser Ser Glu Gln Leu Leu Lys Leu Leu Ser Leu Trp Arg Ile Lys Asn  
 325 330 335  
 Gly Asp Gln Asp Thr Leu Lys Gly Leu Met Tyr Ala Leu Lys His Leu  
 340 345 350

Lys Thr Ser His Phe Pro Lys Thr Val Thr His Ser Leu Arg Lys Thr  
355 360 365

Met Arg Phe Leu His Ser Phe Thr Met Tyr Arg Leu Tyr Gln Lys Leu  
370 375 380

Phe Leu Glu Met Ile Gly Asn Gln Val Gln Ser Val Lys Ile Ser Cys  
385 390 395 400

Leu

<210> 172

<211> 401

<212> PRT

<213> Rattus rattus

<400> 172

Met Asn Lys Trp Leu Cys Cys Ala Leu Leu Val Phe Leu Asp Ile Ile  
1 5 10 15

Glu Trp Thr Thr Gln Glu Thr Phe Pro Pro Lys Tyr Leu His Tyr Asp  
20 25 30

Pro Glu Thr Gly Arg Gln Leu Leu Cys Asp Lys Cys Ala Pro Gly Thr  
35 40 45

Tyr Leu Lys Gln His Cys Thr Val Arg Arg Lys Thr Leu Cys Val Pro  
50 55 60

Cys Pro Asp Tyr Ser Tyr Thr Asp Ser Trp His Thr Ser Asp Glu Cys  
65 70 75 80

Val Tyr Cys Ser Pro Val Cys Lys Glu Leu Gln Thr Val Lys Gln Glu  
85 90 95

Cys Asn Arg Thr His Asn Arg Val Cys Glu Cys Glu Glu Gly Arg Tyr  
100 105 110

Leu Glu Leu Glu Phe Cys Leu Lys His Arg Ser Cys Pro Pro Gly Leu  
115 120 125

Gly Val Leu Gln Ala Gly Thr Pro Glu Arg Asn Thr Val Cys Lys Arg  
130 135 140

Cys Pro Asp Gly Phe Phe Ser Gly Glu Thr Ser Ser Lys Ala Pro Cys  
145 150 155 160

Arg Lys His Thr Asn<sub>165</sub> Cys Ser Ser Leu Gly<sub>170</sub> Leu Leu Leu Ile Gln<sub>175</sub> Lys  
 Gly Asn Ala Thr<sub>180</sub> His Asp Asn Val Cys<sub>185</sub> Ser Gly Asn Arg Glu<sub>190</sub> Ala Thr  
 Gln Asn Cys<sub>195</sub> Gly Ile Asp Val Thr<sub>200</sub> Leu Cys Glu Glu Ala<sub>205</sub> Phe Phe Arg  
 Phe Ala<sub>210</sub> Val Pro Thr Lys Ile<sub>215</sub> Ile Pro Asn Trp Leu<sub>220</sub> Ser Val Leu Val  
 Asp<sub>225</sub> Ser Leu Pro Gly Thr<sub>230</sub> Lys Val Asn Ala Glu<sub>235</sub> Ser Val Glu Arg Ile<sub>240</sub>  
 Lys Arg Arg His Ser<sub>245</sub> Ser Gln Glu Gln Thr<sub>250</sub> Phe Gln Leu Leu Lys<sub>255</sub> Leu  
 Trp Lys His Gln<sub>260</sub> Asn Arg Asp Gln Glu<sub>265</sub> Met Val Lys Lys Ile<sub>270</sub> Ile Gln  
 Asp Ile Asp<sub>275</sub> Leu Cys Glu Ser Ser<sub>280</sub> Val Gln Arg His Ile<sub>285</sub> Gly His Ala  
 Asn Leu<sub>290</sub> Thr Thr Glu Gln Leu<sub>295</sub> Arg Ile Leu Met Glu<sub>300</sub> Ser Leu Pro Gly  
 Lys<sub>305</sub> Lys Ile Ser Pro Asp<sub>310</sub> Glu Ile Glu Arg Thr<sub>315</sub> Arg Lys Thr Cys<sub>320</sub>  
 Pro Ser Glu Gln Leu<sub>325</sub> Leu Lys Leu Leu Ser<sub>330</sub> Leu Trp Arg Ile Lys<sub>335</sub> Asn  
 Gly Asp Gln Asp<sub>340</sub> Thr Leu Lys Gly Leu<sub>345</sub> Met Tyr Ala Leu Lys<sub>350</sub> His Leu  
 Lys Ala Tyr<sub>355</sub> His Phe Pro Lys Thr<sub>360</sub> Val Thr His Ser Leu<sub>365</sub> Arg Lys Thr  
 Ile Arg<sub>370</sub> Phe Leu His Ser Phe<sub>375</sub> Thr Met Tyr Arg Leu<sub>380</sub> Tyr Gln Lys Leu  
 Phe<sub>385</sub> Leu Glu Met Ile Gly<sub>390</sub> Asn Gln Val Gln Ser<sub>395</sub> Val Lys Ile Ser Cys<sub>400</sub>

Leu

<210> 173

&lt;211&gt; 401

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 173

Met Asn Lys Leu Leu Cys Cys Ala Leu Val Phe Leu Asp Ile Ser Ile  
 1 5 10 15

Lys Trp Thr Thr Gln Glu Thr Phe Pro Pro Lys Tyr Leu His Tyr Asp  
 20 25 30

Glu Glu Thr Ser His Gln Leu Leu Cys Asp Lys Cys Pro Pro Gly Thr  
 35 40 45

Tyr Leu Lys Gln His Cys Thr Ala Lys Trp Lys Thr Val Cys Ala Pro  
 50 55 60

Cys Pro Asp His Tyr Tyr Thr Asp Ser Trp His Thr Ser Asp Glu Cys  
 65 70 75 80

Leu Tyr Cys Ser Pro Val Cys Lys Glu Leu Gln Tyr Val Lys Gln Glu  
 85 90 95

Cys Asn Arg Thr His Asn Arg Val Cys Glu Cys Lys Glu Gly Arg Tyr  
 100 105 110

Leu Glu Ile Glu Phe Cys Leu Lys His Arg Ser Cys Pro Pro Gly Leu  
 115 120 125

Gly Val Val Gln Ala Gly Thr Pro Glu Arg Asn Thr Val Cys Lys Arg  
 130 135 140

Cys Pro Asp Gly Phe Phe Ser Asn Glu Thr Ser Ser Lys Ala Pro Cys  
 145 150 155 160

Arg Lys His Thr Asn Cys Ser Val Phe Gly Leu Leu Leu Thr Gln Lys  
 165 170 175

Gly Asn Ala Thr His Asp Asn Ile Cys Ser Gly Asn Ser Glu Ser Thr  
 180 185 190

Gln Lys Cys Gly Ile Asp Val Thr Leu Cys Glu Glu Ala Phe Phe Arg  
 195 200 205

Phe Ala Val Pro Thr Lys Phe Thr Pro Asn Trp Leu Ser Val Leu Val  
 210 215 220

Asp Asn Leu Pro Gly Thr Lys Val Asn Ala Glu Ser Val Glu Arg Ile  
 225 230 235 240

Lys Arg Gln His Ser Ser Gln Glu Gln Thr Phe Gln Leu Leu Lys Leu  
245 250 255

Trp Lys His Gln Asn Lys Asp Gln Asp Ile Val Lys Lys Ile Ile Gln  
260 265 270

Asp Ile Asp Leu Cys Glu Asn Ser Val Gln Arg His Ile Gly His Ala  
275 280 285

Asn Leu Thr Phe Glu Gln Leu Arg Ser Leu Met Glu Ser Leu Pro Gly  
290 295 300

Lys Lys Val Gly Ala Glu Asp Ile Glu Lys Thr Ile Lys Ala Cys Lys  
305 310 315 320

Pro Ser Asp Gln Ile Leu Lys Leu Leu Ser Leu Trp Arg Ile Lys Asn  
325 330 335

Gly Asp Gln Asp Thr Leu Lys Gly Leu Met His Ala Leu Lys His Ser  
340 345 350

Lys Thr Tyr His Phe Pro Lys Thr Val Thr Gln Ser Leu Lys Lys Thr  
355 360 365

Ile Arg Phe Leu His Ser Phe Thr Met Tyr Lys Leu Tyr Gln Lys Leu  
370 375 380

Phe Leu Glu Met Ile Gly Asn Gln Val Gln Ser Val Lys Ile Ser Cys  
385 390 395 400

Leu

<210> 174

<211> 139

<212> PRT

<213> Homo sapiens

<400> 174

Pro Pro Lys Tyr Leu His Tyr Asp Glu Glu Thr Ser His Gln Leu Leu  
1 5 10 15

Cys Asp Lys Cys Pro Pro Gly Thr Tyr Leu Lys Gln His Cys Thr Ala  
20 25 30

Lys Trp Lys Thr Val Cys Ala Pro Cys Pro Asp His Tyr Tyr Thr Asp  
35 40 45

Ser Trp His Thr Ser Asp Glu Cys Leu Tyr Cys Ser Pro Val Cys Lys  
50 55 60

Glu Leu Gln Tyr Val Lys Gln Glu Cys Asn Arg Thr His Asn Arg Val  
65 70 75 80

Cys Glu Cys Lys Glu Gly Arg Tyr Leu Glu Ile Glu Phe Cys Leu Lys  
85 90 95

His Arg Ser Cys Pro Pro Gly Phe Gly Val Val Gln Ala Gly Thr Pro  
100 105 110

Glu Arg Asn Thr Val Cys Lys Arg Cys Pro Asp Gly Phe Phe Ser Asn  
115 120 125

Glu Thr Ser Ser Lys Ala Pro Cys Arg Lys His  
130 135

<210> 175

<211> 380

<212> PRT

<213> Mus musculus

<400> 175

Glu Thr Leu Pro Pro Lys Tyr Leu His Tyr Asp Pro Glu Thr Gly His  
1 5 10 15

Gln Leu Leu Cys Asp Lys Cys Ala Pro Gly Thr Tyr Leu Lys Gln His  
20 25 30

Cys Thr Val Arg Arg Lys Thr Leu Cys Val Pro Cys Pro Asp His Ser  
35 40 45

Tyr Thr Asp Ser Trp His Thr Ser Asp Glu Cys Val Tyr Cys Ser Pro  
50 55 60

Val Cys Lys Glu Leu Gln Ser Val Lys Gln Glu Cys Asn Arg Thr His  
65 70 75 80

Asn Arg Val Cys Glu Cys Glu Glu Gly Arg Tyr Leu Glu Ile Glu Phe  
85 90 95

Cys Leu Lys His Arg Ser Cys Pro Pro Gly Ser Gly Val Val Gln Ala  
100 105 110

Gly Thr Pro Glu Arg Asn Thr Val Cys Lys Lys Cys Pro Asp Gly Phe  
115 120 125



Phe Ser Gly Glu Thr Ser Ser Lys Ala Pro Cys Ile Lys His Thr Asn  
 130 135 140  
 Cys Ser Thr Phe Gly Leu Leu Leu Ile Gln Lys Gly Asn Ala Thr His  
 145 150 155 160  
 Asp Asn Val Cys Ser Gly Asn Arg Glu Ala Thr Gln Lys Cys Gly Ile  
 165 170 175  
 Asp Val Thr Leu Cys Glu Glu Ala Phe Phe Arg Phe Ala Val Pro Thr  
 180 185 190  
 Lys Ile Ile Pro Asn Trp Leu Ser Val Leu Val Asp Ser Leu Pro Gly  
 195 200 205  
 Thr Lys Val Asn Ala Glu Ser Val Glu Arg Ile Lys Arg Arg His Ser  
 210 215 220  
 Ser Gln Glu Gln Thr Phe Gln Leu Leu Lys Leu Trp Lys His Gln Asn  
 225 230 235 240  
 Arg Asp Gln Glu Met Val Lys Lys Ile Ile Gln Asp Ile Asp Leu Cys  
 245 250 255  
 Glu Ser Ser Val Gln Arg His Leu Gly His Ser Asn Leu Thr Thr Glu  
 260 265 270  
 Gln Leu Leu Ala Leu Met Glu Ser Leu Pro Gly Lys Lys Ile Ser Pro  
 275 280 285  
 Glu Glu Ile Glu Arg Thr Arg Lys Thr Cys Lys Ser Ser Glu Gln Leu  
 290 295 300  
 Leu Lys Leu Leu Ser Leu Trp Arg Ile Lys Asn Gly Asp Gln Asp Thr  
 305 310 315 320  
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Asp Trp His  
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